

SEQUENCE LISTING

<110> Svendsen, Allan
Minning, Stefan

<120> Protease Variants

<130> 10517.204-US

<160> 18

<170> PatentIn version 3.3

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Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro	
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tcg cct cat act cct gtt tca agc gat cct tca tac aaa gcg gaa aca	144
Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr	
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tcg gtt act tat gac cca cac att aag agc gat caa tac ggc ttg tat	192
Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr	
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tca aaa gcg ttt aca ggc acc ggc aaa gtg aat gaa aca aag gaa aaa	240
Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys	
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gcg gaa aaa aag tca ccc gcc aaa gct cct tac agc att aaa tcg gtg	288
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Ile	Gly	Ser	Asp	Asp	Arg	Thr	Arg	Val	Thr	Asn	Thr	Thr	Ala	Tyr	Pro		
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tac	aga	gcg	atc	gtt	cat	att	tca	agc	agc	atc	ggt	tca	tgc	acc	gga	384	
Tyr	Arg	Ala	Ile	Val	His	Ile	Ser	Ser	Ser	Ile	Gly	Ser	Cys	Thr	Gly		
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tgg	atg	atc	ggt	ccg	aaa	acc	gtc	gca	aca	gcc	gga	cac	tgc	atc	tat	432	
Trp	Met	Ile	Gly	Pro	Lys	Thr	Val	Ala	Thr	Ala	Gly	His	Cys	Ile	Tyr		
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Asp	Thr	Ser	Ser	Gly	Ser	Phe	Ala	Gly	Thr	Ala	Thr	Val	Ser	Pro	Gly		
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Phe	Ile	Pro	Ser	Gly	Trp	Arg	Ser	Gly	Asn	Thr	Asn	Tyr	Asp	Tyr	Gly		
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gca	atc	gaa	cta	agc	gaa	ccg	atc	ggc	aat	act	gtc	gga	tac	ttc	gga	624	
Ala	Ile	Glu	Leu	Ser	Glu	Pro	Ile	Gly	Asn	Thr	Val	Gly	Tyr	Phe	Gly		
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Tyr	Ser	Tyr	Thr	Thr	Ser	Ser	Leu	Val	Gly	Thr	Thr	Val	Thr	Ile	Ser		
115					120				125						130		
ggc	tac	cca	ggc	gat	aaa	aca	gca	ggc	aca	caa	tgg	cag	cat	tca	gga	720	
Gly	Tyr	Pro	Gly	Asp	Lys	Thr	Ala	Gly	Thr	Gln	Trp	Gln	His	Ser	Gly		
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ccg	att	gcc	atc	tcc	gaa	acg	tat	aaa	ttg	cag	tac	gca	atg	gac	acg	768	
Pro	Ile	Ala	Ile	Ser	Glu	Thr	Tyr	Lys	Leu	Gln	Tyr	Ala	Met	Asp	Thr		
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Tyr	Gly	Gly	Gln	Ser	Gly	Ser	Pro	Val	Phe	Glu	Gln	Ser	Ser	Ser	Arg		
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acg	aac	tgt	agc	ggt	ccg	tgc	tcg	ctt	gcc	gta	cac	aca	aat	gga	gta	864	
Thr	Asn	Cys	Ser	Gly	Pro	Cys	Ser	Leu	Ala	Val	His	Thr	Asn	Gly	Val		
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Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys
 -30 -25 -20 -15

Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val
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Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro
 5 10 15

Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
 20 25 30

Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
 35 40 45 50

Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
 55 60 65

Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
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Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
 85 90 95

Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
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Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
 115 120 125 130

Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
 135 140 145

Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
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Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
 165 170 175

Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
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Ser	Gly	Ile	Leu	Ser	Pro	Val	Asn	Ala	Thr	Gln	Ala	Glu	Thr	Leu	Thr	
-105					-100					-95					-90	
aaa	tta	aat	aaa	ata	agt	cag	aag	cag	gaa	cca	tca	tat	aaa	cta	gat	141
Lys	Leu	Asn	Lys	Ile	Ser	Gln	Lys	Gln	Glu	Pro	Ser	Tyr	Lys	Leu	Asp	
				-85					-80						-75	
gaa	gaa	atg	gat	tat	gtt	cta	att	gat	ttg	gaa	aca	caa	tct	gaa	tcg	189
Glu	Glu	Met	Asp	Tyr	Val	Leu	Ile	Asp	Leu	Glu	Thr	Gln	Ser	Glu	Ser	
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att	att	tcg	ata	gga	gat	aat	acc	gat	ttg	gga	gat	caa	tcg	ttt	act	237
Ile	Ile	Ser	Ile	Gly	Asp	Asn	Thr	Asp	Leu	Gly	Asp	Gln	Ser	Phe	Thr	
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tct	tta	ggg	aag	gtg	gga	cat	gga	gaa	ctt	gag	aaa	att	aac	tta	gaa	285
Ser	Leu	Gly	Lys	Val	Gly	His	Gly	Glu	Leu	Glu	Lys	Ile	Asn	Leu	Glu	
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gaa	ttt	cgt	aat	cct	aat	tta	aca	gta	gta	gac	ccg	tta	aca	cgt	aag	333
Glu	Phe	Arg	Asn	Pro	Asn	Leu	Thr	Val	Val	Asp	Pro	Leu	Thr	Arg	Lys	
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cct	att	gaa	caa	aaa	atc	agc	cct	ttt	gtt	gtt	ata	ggc	gat	gat	ggg	381
Pro	Ile	Glu	Gln	Lys	Ile	Ser	Pro	Phe	Val	Val	Ile	Gly	Asp	Asp	Gly	
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Arg	Arg	Gln	Val	Gln	Asn	Thr	Ser	Phe	Met	Pro	Phe	Arg	Ala	Leu	Thr	
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Tyr	Ile	Glu	Phe	Gly	Asn	Leu	Thr	Ser	Thr	Trp	Ser	Cys	Ser	Gly	Gly	
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gtg	att	gga	aca	gat	tta	gtt	gtt	act	aat	gca	cat	tgt	gta	gaa	ggt	525
Val	Ile	Gly	Thr	Asp	Leu	Val	Val	Thr	Asn	Ala	His	Cys	Val	Glu	Gly	
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tct	gtg	tta	gca	ggt	act	gta	gtt	cct	ggt	atg	aac	aat	agt	cag	tggt	573
Ser	Val	Leu	Ala	Gly	Thr	Val	Val	Pro	Gly	Met	Asn	Asn	Ser	Gln	Trp	
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gca	tat	ggg	cat	tat	agg	gtt	act	cag	att	atc	tac	cct	gat	caa	tac	621
Ala	Tyr	Gly	His	Tyr	Arg	Val	Thr	Gln	Ile	Ile	Tyr	Pro	Asp	Gln	Tyr	
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Arg	Asn	Asn	Gly	Ala	Ser	Glu	Phe	Asp	Tyr	Ala	Ile	Leu	Arg	Val	Ala	
		90					95					100				
cct	gac	tct	gat	gga	cgt	cat	att	gga	aac	aga	gct	gga	att	tta	tct	717
Pro	Asp	Ser	Asp	Gly	Arg	His	Ile	Gly	Asn	Arg	Ala	Gly	Ile	Leu	Ser	

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120	125	130	135
gga tac ccc ggt gat aaa ata tca gag aca aaa tta att tct ttg tgg			813
Gly Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp			
	140	145	150
gga atg gtt ggt cga tct gat gca ttt ttg cat cga gac cta ctg ttc			861
Gly Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe			
	155	160	165
tac aat atg gac acc tat ttt ggt caa tca ggt tct cct gta tta aac			909
Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn			
	170	175	180
agc gta gat tca atg gtt gcg gtt cat aat gca ggg tat atc gtt ggt			957
Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly			
	185	190	195
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Gly Asn Arg Glu Ile Asn Gly Gly Pro Lys Ile Arg Arg Asp Phe Thr			
200	205	210	215
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Lys	Leu	Asn	Lys	Ile	Ser	Gln	Lys	Gln	Glu	Pro	Ser	Tyr	Lys	Leu	Asp
				-85					-80					-75	

Glu	Glu	Met	Asp	Tyr	Val	Leu	Ile	Asp	Leu	Glu	Thr	Gln	Ser	Glu	Ser
			-70					-65					-60		

Ile	Ile	Ser	Ile	Gly	Asp	Asn	Thr	Asp	Leu	Gly	Asp	Gln	Ser	Phe	Thr
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 -25 -20 -15 -10

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Tyr Ile Glu Phe Gly Asn Leu Thr Ser Thr Trp Ser Cys Ser Gly Gly
 25 30 35

Val Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly
 40 45 50 55

Ser Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp
 60 65 70

Ala Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr
 75 80 85

Arg Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala
 90 95 100

Pro Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser
 105 110 115

Phe Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr
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Gly Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp
 140 145 150

Gly Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe
 155 160 165

Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn
 170 175 180

Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly
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 200 205 210 215

Asn Leu Phe Asn Gln Met Asn
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 Ile Ser Ile Phe Ser Ser Gly Ile Tyr Ser Ala Gln Ala Ala Ser Ser
 -75 -70 -65

ccg cat acc cca gtc tcc agc gac cct tcg tac aag ccc ggc tcc acc 144
 Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Gly Ser Thr
 -60 -55 -50 -45

tat gat ccc aac ata aaa att gac aat aac ggc gca tat tcg aaa gcc 192
 Tyr Asp Pro Asn Ile Lys Ile Asp Asn Asn Gly Ala Tyr Ser Lys Ala
 -40 -35 -30

ttc gaa gga acc gga aca ccc ggc ggc tcc gtt cag gcc aaa ccg aaa 240
 Phe Glu Gly Thr Gly Thr Pro Gly Gly Ser Val Gln Ala Lys Pro Lys
 -25 -20 -15

aaa gaa tcg ccc gcc ggc ccg cct tac agc cct aaa tcg gta atc ggc 288
 Lys Glu Ser Pro Ala Gly Pro Pro Tyr Ser Pro Lys Ser Val Ile Gly

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gca atc gtc cat att tca agc agc atc ggc tca tgc aca ggc tgg ctg				384
Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly Trp Leu				
	25	30	35	
atc gga ccg aaa acg gta gca acg gcc ggg cac tgc gtc tat gac acg				432
Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Val Tyr Asp Thr				
	40	45	50	
gca agc cga tca ttc gcg gga acc gcc acc gtt tcc ccg gga cga aac				480
Ala Ser Arg Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly Arg Asn				
	55	60	65	
ggt tca gct tac cct tac gga tct gtt aca tcg acc cgc tat ttc atc				528
Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser Thr Arg Tyr Phe Ile				
	70	75	80	
ccg tcg ggt tgg cag agc gga aat tcc aat tat gac tac gca gcg atc				576
Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr Asp Tyr Ala Ala Ile				
	85	90	95	100
gag ctc agc cag ccg atc ggc aat acc gtc gga tat ttc gga tat tca				624
Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr Ser				
	105	110	115	
tac acc gct tca tcg ctt gca gga gca ggc gtg acc atc agc gga tat				672
Tyr Thr Ala Ser Ser Leu Ala Gly Ala Gly Val Thr Ile Ser Gly Tyr				
	120	125	130	
cca gga gac aaa aca aca ggc acc cag tgg caa atg tcc gga acg atc				720
Pro Gly Asp Lys Thr Thr Gly Thr Gln Trp Gln Met Ser Gly Thr Ile				
	135	140	145	
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Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile Asp Thr Tyr Gly				
	150	155	160	
ggt caa agc ggt tcc ccg gta tat gag aaa agc agt tca agg aca aac				816
Gly Gln Ser Gly Ser Pro Val Tyr Glu Lys Ser Ser Ser Arg Thr Asn				
	165	170	175	180
tgc agc ggc cca tgc tcg ctg gcc gtt cat acg aac ggc gtg tac gga				864
Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val Tyr Gly				
	185	190	195	
gga tcc tct tac aac aga ggc acc cgc att acg aaa gaa gta ttt gat				912
Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val Phe Asp				
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 -60 -55 -50 -45

Tyr Asp Pro Asn Ile Lys Ile Asp Asn Asn Gly Ala Tyr Ser Lys Ala
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Phe Glu Gly Thr Gly Thr Pro Gly Gly Ser Val Gln Ala Lys Pro Lys
 -25 -20 -15

Lys Glu Ser Pro Ala Gly Pro Pro Tyr Ser Pro Lys Ser Val Ile Gly
 -10 -5 -1 1

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Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly Trp Leu
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Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Val Tyr Asp Thr
 40 45 50

Ala Ser Arg Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly Arg Asn
 55 60 65

Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser Thr Arg Tyr Phe Ile
 70 75 80

Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr Asp Tyr Ala Ala Ile
 85 90 95 100

Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr Ser
105 110 115

Tyr Thr Ala Ser Ser Leu Ala Gly Ala Gly Val Thr Ile Ser Gly Tyr
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Pro Gly Asp Lys Thr Thr Gly Thr Gln Trp Gln Met Ser Gly Thr Ile
135 140 145

Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile Asp Thr Tyr Gly
150 155 160

Gly Gln Ser Gly Ser Pro Val Tyr Glu Lys Ser Ser Ser Arg Thr Asn
165 170 175 180

Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val Tyr Gly
185 190 195

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acg tct gat tat gac atg gtg act tct gat gga aag gtg atc tct tca	144														
Thr Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser															
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agt gat ttc cac aat gat acg aaa tcc ccc tca tcc ttt gat aaa gtg	192														
Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Ser Phe Asp Lys Val															
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gat gat cta tct tca act gtt ggt gaa aaa gta aaa cca cta tca aaa	240														
Asp Asp Leu Ser Ser Thr Val Gly Glu Lys Val Lys Pro Leu Ser Lys															
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tat tta aaa gac ttt caa aca aaa gtc gtc att gga gac gat ggt aga	288														
Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg															
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aca aaa gta gca aat aca aga gtg gca cca tat aat tca att gct tat	336														
Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr															
10 15 20															
act acg ttt ggc ggc tcc agc tgc acg ggg acc ctg att gcc cct aac	384														
Thr Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn															
25 30 35 40															
aaa att ttg aca aac gga cac tgc gtg tac aat aca gca tcc aga agt	432														
Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser															
45 50 55															
tat agt gca aaa gga tcg gtg tat cca ggc atg aat gat agt act gcg	480														
Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala															
60 65 70															
gtg aat ggc tca gca aat atg aca gag ttc tat gta cca agc ggg tat	528														
Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr															
75 80 85															
atc aat aca ggt gcg agc caa tat gat ttt gcc gtg atc aaa aca gat	576														
Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp															
90 95 100															
acg aac att ggc aat aca gtt ggt tac cgt tcc atc cgt cag gtg aca	624														
Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr															
105 110 115 120															
aac tta act ggg aca acg att aaa att tct gga tat cca ggt gat aaa	672														
Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys															
125 130 135															
atg aga tca act ggc aag atc tcg cag tgg gag atg tca ggt cct gtg	720														
Met Arg Ser Thr Gly Lys Ile Ser Gln Trp Glu Met Ser Gly Pro Val															
140 145 150															

aca	aga	gaa	gat	acg	aat	ctc	gca	tac	tat	atg	att	gat	aca	ttt	agt	768
Thr	Arg	Glu	Asp	Thr	Asn	Leu	Ala	Tyr	Tyr	Met	Ile	Asp	Thr	Phe	Ser	
		155					160					165				

gga	aat	tca	ggc	tca	gcg	atg	cta	gat	caa	aat	cag	caa	att	gtt	ggg	816
Gly	Asn	Ser	Gly	Ser	Ala	Met	Leu	Asp	Gln	Asn	Gln	Gln	Ile	Val	Gly	
	170					175					180					

gtt	cat	aac	gca	ggg	tat	tca	aac	ggg	acg	att	aat	ggc	ggg	cca	aaa	864
Val	His	Asn	Ala	Gly	Tyr	Ser	Asn	Gly	Thr	Ile	Asn	Gly	Gly	Pro	Lys	
185					190					195					200	

gcg	aca	gct	gcc	ttt	gtt	gaa	ttt	atc	aac	tat	gca	aaa	gcg	caa		909
Ala	Thr	Ala	Ala	Phe	Val	Glu	Phe	Ile	Asn	Tyr	Ala	Lys	Ala	Gln		
				205					210					215		

<210> 8
 <211> 303
 <212> PRT
 <213> Bacillus pumilus BO32

<400> 8

Met	Met	Lys	Lys	Val	Lys	Met	Leu	Leu	Pro	Ser	Leu	Leu	Val	Phe	Gly
		-85					-80						-75		

Ala	Leu	Ser	Val	Pro	Ser	Phe	Ala	His	Ala	Ala	Ser	Asp	Ser	Val	Leu
		-70				-65						-60			

Thr	Ser	Asp	Tyr	Asp	Met	Val	Thr	Ser	Asp	Gly	Lys	Val	Ile	Ser	Ser
	-55				-50						-45				

Ser	Asp	Phe	His	Asn	Asp	Thr	Lys	Ser	Pro	Ser	Ser	Phe	Asp	Lys	Val
-40				-35				-30						-25	

Asp	Asp	Leu	Ser	Ser	Thr	Val	Gly	Glu	Lys	Val	Lys	Pro	Leu	Ser	Lys
		-20					-15						-10		

Tyr	Leu	Lys	Asp	Phe	Gln	Thr	Lys	Val	Val	Ile	Gly	Asp	Asp	Gly	Arg
	-5					-1	1				5				

Thr	Lys	Val	Ala	Asn	Thr	Arg	Val	Ala	Pro	Tyr	Asn	Ser	Ile	Ala	Tyr
10					15					20					

Thr	Thr	Phe	Gly	Gly	Ser	Ser	Cys	Thr	Gly	Thr	Leu	Ile	Ala	Pro	Asn
25					30				35					40	

Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser
45 50 55

Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala
60 65 70

Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr
75 80 85

Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp
90 95 100

Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr
105 110 115 120

Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys
125 130 135

Met Arg Ser Thr Gly Lys Ile Ser Gln Trp Glu Met Ser Gly Pro Val
140 145 150

Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Met Ile Asp Thr Phe Ser
155 160 165

Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly
170 175 180

Val His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys
185 190 195 200

Ala Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln
205 210 215

<210> 9
<211> 954
<212> DNA
<213> Bacillus licheniformis CDJ31

<220>
<221> CDS
<222> (1)..(954)

<220>
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<222> (1)..(84)

<220>
 <221> pro_peptide
 <222> (85)..(288)

<220>
 <221> mat_peptide
 <222> (289)..(954)

<400> 9
 atg aaa aaa agt gtg aca cgc gta tta atg gcc ggt ctt att gga ata 48
 Met Lys Lys Ser Val Thr Arg Val Leu Met Ala Gly Leu Ile Gly Ile
 -95 -90 -85

tct att tat tct atg ggc atc gac tcc gct caa gct gca tca tcg ccg 96
 Ser Ile Tyr Ser Met Gly Ile Asp Ser Ala Gln Ala Ala Ser Ser Pro
 -80 -75 -70 -65

cat act cct gtc tct agc gat cct tca tac aag ccc gac tca tcc gca 144
 His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Asp Ser Ser Ala
 -60 -55 -50

agc tat gat cct gct att aaa acc aac aaa aac ggc gcc tat tca aaa 192
 Ser Tyr Asp Pro Ala Ile Lys Thr Asn Lys Asn Gly Ala Tyr Ser Lys
 -45 -40 -35

gca ttt gaa ggt aca gga aaa cta gac gct ccc ctt tat cag gaa aaa 240
 Ala Phe Glu Gly Thr Gly Lys Leu Asp Ala Pro Leu Tyr Gln Glu Lys
 -30 -25 -20

agc aaa cca acc aaa aaa tcc cct gcc gga cca cgt tac agc ccc aaa 288
 Ser Lys Pro Thr Lys Lys Ser Pro Ala Gly Pro Arg Tyr Ser Pro Lys
 -15 -10 -5 -1

tcc gtg att ggt tct gat gaa cgg acg aga gtg aca aac act acc gca 336
 Ser Val Ile Gly Ser Asp Glu Arg Thr Arg Val Thr Asn Thr Thr Ala
 1 5 10 15

tat cca tac aga gcg atc gtg cat att tca agc agc atc ggg tct tgc 384
 Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys
 20 25 30

acc ggc tcc ctg atc ggt ccg aaa acg gtg gca acg gcc gga cac tgc 432
 Thr Gly Ser Leu Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys
 35 40 45

att tat gac aca gcg agc ggg tca ttc gcc gga acc gct acc gtt tct 480
 Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser
 50 55 60

ccg gga cgg aac ggt tca aca tat ccg tac gga tca gtt aca tca acc 528
 Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser Thr
 65 -70 75 80

cgc tat ttc atc ccg tca ggc tat cga agc gga aat tcg aat tac gac 576
 Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr Asp
 85 90 95

tac gga gcc ata gag ctc agc cag ccg atc ggc aac acc gtc ggg tat	624
Tyr Gly Ala Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr	
100 105 110	
ttc gga tat tcc tac acc acc tcg tct ctc gtt ggg tca agc gtt acc	672
Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Ser Val Thr	
115 120 125	
atc atc gga tat cca ggc gac aaa aca tcg ggc acc caa tgg cag atg	720
Ile Ile Gly Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met	
130 135 140	
tcc gga aat atc gcc gtc tca gaa aca tat aaa ctg caa tat gcg atc	768
Ser Gly Asn Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile	
145 150 155 160	
gac aca tac gga ggg cag agc ggc tct ccc gta tat gag gcg agc agc	816
Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Tyr Glu Ala Ser Ser	
165 170 175	
tcc aga acg aat tgc agc ggc cca tgt tcg ctg gcc gtt cat acg aat	864
Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn	
180 185 190	
ggg gtg tac gga gga tct tca tac aac aga ggc acc cgg att aca aaa	912
Gly Val Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys	
195 200 205	
gaa gta ttc gat aat ttg aca aac tgg aaa aac agc gcc caa	954
Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln	
210 215 220	

<210> 10
 <211> 318
 <212> PRT
 <213> Bacillus licheniformis CDJ31

<400> 10

Met Lys Lys Ser Val Thr Arg Val Leu Met Ala Gly Leu Ile Gly Ile
-95 -90 -85

Ser Ile Tyr Ser Met Gly Ile Asp Ser Ala Gln Ala Ala Ser Ser Pro
-80 -75 -70 -65

His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Asp Ser Ser Ala
-60 -55 -50

Ser Tyr Asp Pro Ala Ile Lys Thr Asn Lys Asn Gly Ala Tyr Ser Lys
-45 -40 -35

Ala Phe Glu Gly Thr Gly Lys Leu Asp Ala Pro Leu Tyr Gln Glu Lys
 -30 -25 -20

Ser Lys Pro Thr Lys Lys Ser Pro Ala Gly Pro Arg Tyr Ser Pro Lys
 -15 -10 -5 -1

Ser Val Ile Gly Ser Asp Glu Arg Thr Arg Val Thr Asn Thr Thr Ala
 1 5 10 15

Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys
 20 25 30

Thr Gly Ser Leu Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys
 35 40 45

Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser
 50 55 60

Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser Thr
 65 70 75 80

Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr Asp
 85 90 95

Tyr Gly Ala Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr
 100 105 110

Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Ser Val Thr
 115 120 125

Ile Ile Gly Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met
 130 135 140

Ser Gly Asn Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile
 145 150 155 160

Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Tyr Glu Ala Ser Ser
 165 170 175

Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn
 180 185 190

Gly Val Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys

195

200

205

Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
 210 215 220

<210> 11
 <211> 906
 <212> DNA
 <213> Bacillus pumilus JA96

<220>
 <221> CDS
 <222> (1)..(906)

<220>
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<220>
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 <222> (76)..(261)

<220>
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 <222> (262)..(906)

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 atg aaa aag gtg aaa aaa tta atc cct tct cta ctc gtt ttt ggt gct 48
 Met Lys Lys Val Lys Lys Leu Ile Pro Ser Leu Leu Val Phe Gly Ala
 -85 -80 -75

tta agt gtg cct agt ttt gcc cat gca gca tct gat tca gta ctt acg 96
 Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu Thr
 -70 -65 -60

tct gat tat gac atg gtg act tct gac gga aag gtg att tct tca gct 144
 Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser Ala
 -55 -50 -45 -40

gac ttc cac aac gat atg aaa acc ccc tca tcc ttt gac aaa gtg gat 192
 Asp Phe His Asn Asp Met Lys Thr Pro Ser Ser Phe Asp Lys Val Asp
 -35 -30 -25

gat ctc tct tct act att ggc gaa aaa gta aaa cca ctc aca aca tat 240
 Asp Leu Ser Ser Thr Ile Gly Glu Lys Val Lys Pro Leu Thr Thr Tyr
 -20 -15 -10

tta aaa gac ttt caa aca aaa gta gtc att gga gac gat ggt aga aca 288
 Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg Thr
 -5 -1 1 5

aaa gtg acg aat aca aga gta gca ccc tat aat tct att gct tat att 336
 Lys Val Thr Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr Ile
 10 15 20 25

aca ttt ggt gga tct agc tgc act gga aca ctc att gct cca aac aaa	384
Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn Lys	
30 35 40	
ata ttg aca aac gga cac tgc gtc tac aat aca gcc aca aga agt tat	432
Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Thr Arg Ser Tyr	
45 50 55	
agt gca aaa ggg tct gtc tac cca ggc atg aat gac agc acg gct gtg	480
Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala Val	
60 65 70	
aac ggc tca gca aac atg acc gaa ttc tat gta cca agc gga tat atc	528
Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr Ile	
75 80 85	
aac acg ggg gcg agt caa tat gat ttt gcc gtc att aaa aca gat acg	576
Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp Thr	
90 95 100 105	
aac att gga aat acg gtc ggc tat cgc tct att cgt caa gtg aca aat	624
Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr Asn	
110 115 120	
cta aca ggt aca acg att aaa att tct gga tat cca ggt gat aaa atg	672
Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys Met	
125 130 135	
aga tcg act ggc aaa gtg tca caa tgg gaa atg tca ggt cca gtc acg	720
Arg Ser Thr Gly Lys Val Ser Gln Trp Glu Met Ser Gly Pro Val Thr	
140 145 150	
aga gaa gat acg aat ctc gca tac tat acg atc gat aca ttt agc gga	768
Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser Gly	
155 160 165	
aac tct ggc tct gcg atg cta gat cag aac caa caa atc gtc ggg gtc	816
Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly Val	
170 175 180 185	
cat aat gcg ggt tat tca aat gga acg atc aac ggt gga cca aaa gcg	864
His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys Ala	
190 195 200	
act gct gcc ttt gtt gaa ttt atc aac tat gcg aag gcg caa	906
Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln	
205 210 215	

<210> 12
 <211> 302
 <212> -PRT
 <213> Bacillus pumilus JA96

<400> 12

Met Lys Lys Val Lys Lys Leu Ile Pro Ser Leu Leu Val Phe Gly Ala
 -85 -80 -75

Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu Thr
 -70 -65 -60

Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser Ala
 -55 -50 -45 -40

Asp Phe His Asn Asp Met Lys Thr Pro Ser Ser Phe Asp Lys Val Asp
 -35 -30 -25

Asp Leu Ser Ser Thr Ile Gly Glu Lys Val Lys Pro Leu Thr Thr Tyr
 -20 -15 -10

Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg Thr
 -5 -1 1 5

Lys Val Thr Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr Ile
 10 15 20 25

Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn Lys
 30 35 40

Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Thr Arg Ser Tyr
 45 50 55

Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala Val
 60 65 70

Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr Ile
 75 80 85

Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp Thr
 90 95 100 105

Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr Asn
 110 115 120

Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys Met
 125 130 135

Arg Ser Thr Gly Lys Val Ser Gln Trp Glu Met Ser Gly Pro Val Thr

140	145	150
Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser Gly		
155	160	165
Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly Val		
170	175	180
His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys Ala		
190	195	200
Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln		
205	210	215

<210> 13
 <211> 939
 <212> DNA
 <213> Bacillus subtilis IS75

<220>
 <221> CDS
 <222> (1)..(939)

<220>
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 <222> (1)..(102)

<220>
 <221> pro_peptide
 <222> (103)..(279)

<220>
 <221> mat_peptide
 <222> (280)..(939)

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Met Lys Leu Val Pro Arg Phe Arg Lys Gln Trp Phe Ala Tyr Leu Thr	
-90 -85 -80	
gtt ttg tgt ttg gct ttg gca gca gcg gtt tct ttt ggc gta ccg gca	96
Val Leu Cys Leu Ala Leu Ala Ala Ala Val Ser Phe Gly Val Pro Ala	
-75 -70 -65	
aaa gcg gca gag aac ccg caa act tct gta tcg aat acc ggt aaa gaa	144
Lys Ala Ala Gly Asn Pro Gln Thr Ser Val Ser Asn Thr Gly Lys Glu	
-60 -55 -50	
gct gat gct acg aaa aac caa acg tca aaa gca gat cag gtt tcc gcc	192
Ala Asp Ala Thr Lys Asn Gln Thr Ser Lys Ala Asp Gln Val Ser Ala	
-45 -40 -35 -30	

cct tat gag gga acc gga aaa aca agt aaa tcg tta tac ggc ggc caa	240
Pro Tyr Glu Gly Thr Gly Lys Thr Ser Lys Ser Leu Tyr Gly Gly Gln	
-25 -20 -15	
acg gaa ctg gaa aaa aac att caa acc tta cag cct tcg agc att atc	288
Thr Glu Leu Glu Lys Asn Ile Gln Thr Leu Gln Pro Ser Ser Ile Ile	
-10 -5 -1 1	
gga act gat gaa cgc acc aga atc tcc agc acg aca tct ttt cca tat	336
Gly Thr Asp Glu Arg Thr Arg Ile Ser Ser Thr Thr Ser Phe Pro Tyr	
5 10 15	
aga gca acc gtt caa ctg tca atc aag tat ccc aac act tca agc act	384
Arg Ala Thr Val Gln Leu Ser Ile Lys Tyr Pro Asn Thr Ser Ser Thr	
20 25 30 35	
tat gga tgt acc gga ttt tta gtc aat cca aat aca gtc gtc acg gct	432
Tyr Gly Cys Thr Gly Phe Leu Val Asn Pro Asn Thr Val Val Thr Ala	
40 45 50	
gga cat tgt gtg tac agc cag gat cat gga tgg gct tcg acg ata acc	480
Gly His Cys Val Tyr Ser Gln Asp His Gly Trp Ala Ser Thr Ile Thr	
55 60 65	
gcc gcg ccg ggc cgc aat ggt tcg tca tat ccg tac ggt act tat tca	528
Ala Ala Pro Gly Arg Asn Gly Ser Ser Tyr Pro Tyr Gly Thr Tyr Ser	
70 75 80	
ggc acg atg ttt tac tcc gtc aaa gga tgg acg gaa agc aaa gac acc	576
Gly Thr Met Phe Tyr Ser Val Lys Gly Trp Thr Glu Ser Lys Asp Thr	
85 90 95	
aac tat gat tac gga gct att aaa tta aac ggt tct cct gga aac acg	624
Asn Tyr Asp Tyr Gly Ala Ile Lys Leu Asn Gly Ser Pro Gly Asn Thr	
100 105 110 115	
gtt ggc tgg tac ggc tac cgg act aca aac agc agc agt ccc gtg ggc	672
Val Gly Trp Tyr Gly Tyr Arg Thr Thr Asn Ser Ser Ser Pro Val Gly	
120 125 130	
ctt tcc tcg tca gtg aca gga ttc cca tgt gac aaa acc ttt ggc acg	720
Leu Ser Ser Ser Val Thr Gly Phe Pro Cys Asp Lys Thr Phe Gly Thr	
135 140 145	
atg tgg tct gat aca aag ccg att cgc tcc gct gaa acg tat aag ctg	768
Met Trp Ser Asp Thr Lys Pro Ile Arg Ser Ala Glu Thr Tyr Lys Leu	
150 155 160	
acc tat aca acc gat acg tac ggc tgc caa agc ggc tcg cct gtt tat	816
Thr Tyr Thr Thr Asp Thr Tyr Gly Cys Gln Ser Gly Ser Pro Val Tyr	
165 170 175	
cga aac tac agt gat aca ggg cag aca gct att gcc att cac acg aac	864
Arg Asn Tyr Ser Asp Thr Gly Gln Thr Ala Ile Ala Ile His Thr Asn	
180 185 190 195	

gga gga tcg tca tat aac ttg gga aca agg gtg acg aac gat gta ttc 912
 Gly Gly Ser Ser Tyr Asn Leu Gly Thr Arg Val Thr Asn Asp Val Phe
 200 205 210

aac aat att caa tat tgg gca aat caa 939
 Asn Asn Ile Gln Tyr Trp Ala Asn Gln
 215 220

<210> 14
 <211> 313
 <212> PRT
 <213> Bacillus subtilis IS75

<400> 14

Met Lys Leu Val Pro Arg Phe Arg Lys Gln Trp Phe Ala Tyr Leu Thr
 -90 -85 -80

Val Leu Cys Leu Ala Leu Ala Ala Val Ser Phe Gly Val Pro Ala
 -75 -70 -65

Lys Ala Ala Glu Asn Pro Gln Thr Ser Val Ser Asn Thr Gly Lys Glu
 -60 -55 -50

Ala Asp Ala Thr Lys Asn Gln Thr Ser Lys Ala Asp Gln Val Ser Ala
 -45 -40 -35 -30

Pro Tyr Glu Gly Thr Gly Lys Thr Ser Lys Ser Leu Tyr Gly Gly Gln
 -25 -20 -15

Thr Glu Leu Glu Lys Asn Ile Gln Thr Leu Gln Pro Ser Ser Ile Ile
 -10 -5 -1 1

Gly Thr Asp Glu Arg Thr Arg Ile Ser Ser Thr Thr Ser Phe Pro Tyr
 5 10 15

Arg Ala Thr Val Gln Leu Ser Ile Lys Tyr Pro Asn Thr Ser Ser Thr
 20 25 30 35

Tyr Gly Cys Thr Gly Phe Leu Val Asn Pro Asn Thr Val Val Thr Ala
 40 45 50

Gly His Cys Val Tyr Ser Gln Asp His Gly Trp Ala Ser Thr Ile Thr
 55 60 65

Ala Ala Pro Gly Arg Asn Gly Ser Ser Tyr Pro Tyr Gly Thr Tyr Ser

70					75					80					
Gly	Thr	Met	Phe	Tyr	Ser	Val	Lys	Gly	Trp	Thr	Glu	Ser	Lys	Asp	Thr
85					90					95					
Asn	Tyr	Asp	Tyr	Gly	Ala	Ile	Lys	Leu	Asn	Gly	Ser	Pro	Gly	Asn	Thr
100					105					110					115
Val	Gly	Trp	Tyr	Gly	Tyr	Arg	Thr	Thr	Asn	Ser	Ser	Ser	Pro	Val	Gly
				120					125					130	
Leu	Ser	Ser	Ser	Val	Thr	Gly	Phe	Pro	Cys	Asp	Lys	Thr	Phe	Gly	Thr
			135					140					145		
Met	Trp	Ser	Asp	Thr	Lys	Pro	Ile	Arg	Ser	Ala	Glu	Thr	Tyr	Lys	Leu
		150					155					160			
Thr	Tyr	Thr	Thr	Asp	Thr	Tyr	Gly	Cys	Gln	Ser	Gly	Ser	Pro	Val	Tyr
	165					170					175				
Arg	Asn	Tyr	Ser	Asp	Thr	Gly	Gln	Thr	Ala	Ile	Ala	Ile	His	Thr	Asn
180					185					190					195
Gly	Gly	Ser	Ser	Tyr	Asn	Leu	Gly	Thr	Arg	Val	Thr	Asn	Asp	Val	Phe
				200					205					210	
Asn	Asn	Ile	Gln	Tyr	Trp	Ala	Asn	Gln							
			215					220							

<210> 15
 <211> 909
 <212> DNA
 <213> Bacillus intermedius

<220>
 <221> CDS
 <222> (1)..(909)

<220>
 <221> sig_peptide
 <222> (1)..(78)

<220>
 <221> pro_peptide
 <222> (79)..(264)

<220>

<221> mat_peptide

<222> (265)..(909)

<400> 15

atg atg aaa aag gtg aaa atg tta ctc cct tct cta ctc gtt ttt ggt 48
Met Met Lys Lys Val Lys Met Leu Leu Pro Ser Leu Leu Val Phe Gly

-85

-80

-75

gct tta agt gtg cct agt ttt gcc cat gcc aca tcg gat tca gta cta 96
Ala Leu Ser Val Pro Ser Phe Ala His Ala Thr Ser Asp Ser Val Leu

-70

-65

-60

acg tct gat tat gac atg gtg act tct gat gga aag gtg atc tct tca 144
Thr Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser

-55

-50

-45

agt gat ttc cac aat gat acg aaa tcc ccc tca tcc ttt gac aaa gtg 192
Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Ser Phe Asp Lys Val

-40

-35

-30

-25

gat gat ctt tct tct act tct ggc gaa aaa gta aaa cca ctc tca aaa 240
Asp Asp Leu Ser Ser Thr Ser Gly Glu Lys Val Lys Pro Leu Ser Lys

-20

-15

-10

tat tta aaa gac ttt caa aca aaa gtc gtc att gga gac gat gga ada 288
Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Xaa

-5

-1

1

5

aca aaa gta gca aac aca aga gtg gca cca tat aat tca att gct tat 336
Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr

10

15

20

att aca ttt ggc ggc tca agc tgc acg ggg aca ctc att gcc cct aac 384
Ile Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn

25

30

35

40

aaa att ttg aca aac ggc cac tgc gtg tac aat aca gca tcg aga agt 432
Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser

45

50

55

tat agt gca aaa gga tcg gtg tat cca ggc atg aac gat agt aca gcg 480
Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala

60

65

70

gtg aat ggc tca gca aac atg acg gag ttc tat gta cca agc gga tat 528
Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr

75

80

85

atc aat aca ggc gcg agc caa tat gat ttt gcc gtg atc aaa aca gat 576
Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp

90

95

100

acg aac att ggc aat acg gtc ggt tac cgc tct atc cgt cag gtg aca 624
Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr

105

110

115

120

aac tta act ggg aca acg att aaa att tct gga tat cca ggt gat aaa	672
Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys	
125 130 135	
atg ada tcg act ggc aag gtg tcg cad tgg gag atg tca ggt tct gtg	720
Met Xaa Ser Thr Gly Lys Val Ser Xaa Trp Glu Met Ser Gly Ser Val	
140 145 150	
aca aga gaa gat aca aat ctc gca tac tat acg att gat aca ttt agc	768
Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser	
155 160 165	
gga aat tca ggc tca gcg atg cta gat caa aat cad caa atc gtt ggg	816
Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Xaa Gln Ile Val Gly	
170 175 180	
gtt cat aac gca ggg tat tca aac gga acg att aat ggc ggt cca aaa	864
Val His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys	
185 190 195 200	
gcg aca gct gcc ttt gtt gaa ttt atc aac tat gca aaa gcg caa	909
Ala Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln	
205 210 215	

<210> 16
 <211> 303
 <212> PRT
 <213> Bacillus intermedius

<220>
 <221> misc_feature
 <222> (8)..(8)
 <223> The 'Xaa' at location 8 stands for Lys, Arg, or Ile.

<220>
 <221> misc_feature
 <222> (138)..(138)
 <223> The 'Xaa' at location 138 stands for Lys, Arg, or Ile.

<220>
 <221> misc_feature
 <222> (145)..(145)
 <223> The 'Xaa' at location 145 stands for Gln, or His.

<220>
 <221> misc_feature
 <222> (180)..(180)
 <223> The 'Xaa' at location 180 stands for Gln, or His.

<400> 16

Met Met Lys Lys Val Lys Met Leu Leu Pro Ser Leu Leu Val Phe Gly
-85 -80 -75

Ala Leu Ser Val Pro Ser Phe Ala His Ala Thr Ser Asp Ser Val Leu

-70					-65					-60					
Thr	Ser	Asp	Tyr	Asp	Met	Val	Thr	Ser	Asp	Gly	Lys	Val	Ile	Ser	Ser
	-55					-50					-45				
Ser	Asp	Phe	His	Asn	Asp	Thr	Lys	Ser	Pro	Ser	Ser	Phe	Asp	Lys	Val
-40				-35					-30						-25
Asp	Asp	Leu	Ser	Ser	Thr	Ser	Gly	Glu	Lys	Val	Lys	Pro	Leu	Ser	Lys
			-20					-15					-10		
Tyr	Leu	Lys	Asp	Phe	Gln	Thr	Lys	Val	Val	Ile	Gly	Asp	Asp	Gly	Xaa
		-5				-1	1				5				
Thr	Lys	Val	Ala	Asn	Thr	Arg	Val	Ala	Pro	Tyr	Asn	Ser	Ile	Ala	Tyr
	10				15						20				
Ile	Thr	Phe	Gly	Gly	Ser	Ser	Cys	Thr	Gly	Thr	Leu	Ile	Ala	Pro	Asn
25				30					35						40
Lys	Ile	Leu	Thr	Asn	Gly	His	Cys	Val	Tyr	Asn	Thr	Ala	Ser	Arg	Ser
			45					50						55	
Tyr	Ser	Ala	Lys	Gly	Ser	Val	Tyr	Pro	Gly	Met	Asn	Asp	Ser	Thr	Ala
		60					65					70			
Val	Asn	Gly	Ser	Ala	Asn	Met	Thr	Glu	Phe	Tyr	Val	Pro	Ser	Gly	Tyr
	75					80					85				
Ile	Asn	Thr	Gly	Ala	Ser	Gln	Tyr	Asp	Phe	Ala	Val	Ile	Lys	Thr	Asp
	90				95						100				
Thr	Asn	Ile	Gly	Asn	Thr	Val	Gly	Tyr	Arg	Ser	Ile	Arg	Gln	Val	Thr
105				110					115						120
Asn	Leu	Thr	Gly	Thr	Thr	Ile	Lys	Ile	Ser	Gly	Tyr	Pro	Gly	Asp	Lys
			125					130					135		
Met	Xaa	Ser	Thr	Gly	Lys	Val	Ser	Xaa	Trp	Glu	Met	Ser	Gly	Ser	Val
			140				145					150			
Thr	Arg	Glu	Asp	Thr	Asn	Leu	Ala	Tyr	Tyr	Thr	Ile	Asp	Thr	Phe	Ser
	155					160						165			

Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Xaa Gln Ile Val Gly
170 175 180

Val His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys
185 190 195 200

Ala Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln
205 210 215

<210> 17
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 17
ctgtgccctt taaccgcaca gc

22

<210> 18
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 18
gcataagctt ttacaggtac cggc

24